

**FIGURE 1**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGCTTCAGCCTGA  
AGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCTTGGCCTCCAACTTGTGGG  
CTACATCCTAGGCCTCTGGGCTTTGGGCACACTGGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTA  
TGTCGGTGCCAGCATTGTGACAGCAGTGGCTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGG  
CATCACCCAGTGTGACATCTATAGCACCCCTCTGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGT  
GACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCACAGTCTTCTGCCAGGA  
ATCCCGAGCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTGGAGGCCTCTGGATTCAATTCC  
TGTTGCCTGGAATCTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAGCATGAAATTGAGAT  
TGGAGAGGCTTTACTGGCATTATTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTG  
CTCATCCCAGAGAAATCGCTCCAACTAACGATGCCAACCTCTGCCACAAGGAGCTCTCCAAG  
GCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGTATGTGTGAAGAACCCAGGG  
CCAGAGCTGGGGGTGGCTGGCTGTGAAAAACAGTGGACAGCACCCGAGGCCACAGGTGAGGGACACTACC  
ACTGGATCGTGTCAAGAGGTGCTGCTGAGGATAGACTGACTTGGCATTGGATTGAGCAAAGGCAGAAATGGGG  
GCTAGTGTAAACAGCATGCAAGGTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTTCCTCACCTGCT  
GCTCCCTGCCCTAACGCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGGATCCCTTG  
CCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAACATCACATCCCACGTGACTGACCCCTGTGATCAAAGA  
CCCTCTCTGGCTGAGGTTGGCTCTAGCTCATTGCTGGGATGGAAGGAGAACGAGTGGCTTTGTGGCAT  
TGCTCTAACCTACTTCTCAAGCTTCCCTCAAAGAAACTGATTGGCCTGGAACCTCCACTCTGTTATG  
ACTCCACAGTGTCCAGACTAATTGTGCACTGAAATAAAACCATCCTACGGTATCCAGGAAACAGAAAGCA  
GGATGCAGGATGGGAGGACAGGAAGGCAGCCTGGACATTAAAAAAATA

**FIGURE 2**

GAGAGAGGCAGCAGCTGCTCAGCGAACAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACCTGGGCCT  
 CCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGCCAGGCCAGGACCTGTGAGGGAGGCCCTCCTGCTGC  
 CTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTG  
 ACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGAACACCCGTATCCCATGGAGACCTTCAGAA  
 AGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTTGTCTCATCAAGGTGA  
 TTCTGGATAAATACTACTTCCTCTGCAGGCTCCACTTCATCCCGAGGAAGCAGCTGTGACGGAGAGC  
 TGGACTGTCCCTGGGGAGGACGAGGAGCACTGTGTCAGAGCTTCCGAAGGGCCTGCAGTGGCAGTCCGCC  
 TCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGAACGGTTCTGCCTGTTGACA  
 TCACAGAAGCTCGCTGAGACAGCCTGTAGGCAGATGGCCTACAGCAGAGCTGTGGAGATTGGCCAGACAGG  
 ATCTGGATGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACACTCAAGTGGCCCTGTCTCAG  
 GCTCCCTGGTCTCCCTGCACTGTCTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGAGGAGG  
 CCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGG  
 ACCCCCCACTGGGCCTCACGGCAGCCCAGTCTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCCAGG  
 GCTCAGACAAACTGGCAGCTTCCATCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACC  
 CCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCACTCACTTCTCAGGCACAGTCAGGCCATCTGTC  
 TGCCCTTCTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGATGGGCTTACGAAGCAGAAATG  
 GAGGGAAAGATGTCACATACTGCTGCAGGCGTCAGTCCAGGTGATTGACAGCACACGGTCAATGCAGACGATG  
 CGTACCAAGGGGAAGTCACCGAGAAGATGATGTGTCAGGCATCCGGAAAGGGGGTGTGGACACCTGCCAGGGTG  
 ACAGTGGTGGGCCCTGATGTACCAATCTGACCAAGTGGCATGTGGTGGCATCGTAGCTGGGCTATGGCTGCG  
 GGGGCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTG  
**AGCTG****TAAT**GCTGCTGCCCTTGCAGTGCAGGAGCCCTTCCCTGCCCTGCCACCTGGGATCCCCAA  
 AGTCAGACACAGAGCAAGAGTCCCCTGGTACACCCCTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAG  
 GGCCCTCAATTCTGTAAAGAGACCCCTCGCAGGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTGCCACAC  
 TTGGTGCTCCAGCATCCAGGGAGAGACACAGCCCAGTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAAGG  
 AACCTTCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAGCCCAGATCACTGTGGCTGGAGAGGAGAAGG  
 AAAGGGTCTGCCAGCCCTGTCGTCTCACCCATCCCCAGCCTACTAGAGCAAGAAACCAGTTGTAATATAA  
 AATGCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGCCACTATTA  
 TAAAGAGCTGTGTAACATCTGGCAAAAAAAAAAAAAA

### **FIGURE 3**

GGAGGGCAGCGGAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCAGCCATGGCTTCCCTGGG  
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT  
ATTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC  
TGCACCTTGAAACCTGACATCAAACCTTCTGATATCGTACATACAATGGCTGAAGGAAGGTGTTTAGGCTTGGTC  
CATGAGTTCAAAGAAGGCAAAGATGAGCTGTCGGAGCAGGATGAAATGTTAGGGCCGGACAGCAGTGTGCT  
GATCAAGTGATAGTGGCAATGCCCTTTGCGGCTGAAAAACGTGCAAACACAGATGCTGGCACCTACAAATGT  
TATATCATCACTCTAAAGGCAAGGGGATGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCCGGAAAGTG  
AATGTGGACTATAATGCCAGCTCAGAGACCTGCGGTGTGAGGCTCCCCGATGGTCCCCAGCCCACAGTGGTC  
TGGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTGAGCTGAACCTGAGAAT  
GTGACCATGAAGGTTGTGCTGTGCTACAATGTTACGATCAACAAACACATACTCCTGTATGATTGAAAATGAC  
ATTGCCAAAGCAACAGGGATATCAAAGTGACAGAACTGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAC  
TCAAAGGCTCTGTGTCTTCTTCTTGCCATCAGCTGGCACTTCTGCCTCTAGCCCTTACCTGATG  
CTAAAATATGTGCCTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAGATATGACCTAGTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAG  
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCAAATATGAACAAGATAATCTATCTCAAAGACATATTA  
GAAGTTGGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAATGCACGTGGAGACAAGT  
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGAGTGAGAGGACAGGATAGTCATGTTCTTG  
TCTCTGAATTAGTTAGTTATGTGCTGTAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCAAACATATCCA  
CATCTTATATTCCACAAATTAGCTGTAGTATGTACCCCTAACAGCCTGCTAACAGACTGCCACTCGCAACTCAG  
GGGCGGCTGCATTAGTAATGGGTCAAATGATTCACTTTTATGATGCTTCCAAAGGTGCCTGGCTCTTC  
CCAAGTGCACAAATGCCAAAGTTGAGAAAAATGATCATATTAGCATAAACAGAGCAGTCGGGACACCGATT  
TATAAAATAAACTGAGCACCTTCTTTAAACAAAAA  
AAAAAAAAA

**FIGURE 4**

TGCCGGGCTGCGGGCGCCTGACTCTCCCTCACCCCTGCCTCCTCGGGCTCCACTCGTCTGCCCTGGACTCCC  
 GTCTCCTCCTGTCCTCCGGCTCCCAGAGCTCCCTCCTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT  
 CAGCGGACGACCCCTCGCTCCGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG  
 TTTGGCTGCTGCTTCCCACCGCCGCGCTGCACTGCCACCGCCGCCCTGCTGCCGCCGTCGGGATGCTCAG  
 TAGCCCCTGCCCGCCCCCGCGATCCTGTGTTCTCGGAAGCCGTTGCTGCTGCAGAGTTGCACGAACTAGTC  
**ATG**GTGCTGTTGGAGTCCCACCGCAGTGCAGCAGCTGGACACTTGCAGGGCTTGCTGGCTGCTGCTGCTG  
 CCCGTCACTGCTACTCATCGTAGCCCACCGCAGTGCAGCAGCTGGACACTTGCAGGGCTTGCTGGCTGCTGCTG  
 CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTCCTGACACCAACACCTGTA  
 TTTGATGGGAATGTTAAGAATTGGAGACACTGTGACTTGCCTGTCAGTTCAAGTGCACAAATGACTATG  
 CCTGTGTGTGGCTCCAATGGGAGAGCTACAGAATGAGTGTACCTGCGACAGGCTGCATGCAAACAGCAGAGT  
 GAGATACTGTGGTGTCAAGAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGG  
 TCTGGAGAAAATAGTCAAAAGGAGACATCCACCTGTGATATTGCCAGTTGGTGCAGAATGTGACGAAGATGCC  
 GAGGATGTCTGGTGTGTGTAATATTGACTGTTCTAAACCAACTTCATCCCCTGCGCTTCTGATGGGAA  
 TCTTATGATAATGCATGCCAAATCAAAGAACATCGTCAGAACAGGAGAAAATTGAAGTCATGTTGGGT  
 CGATGTCAAGATAACACAACTACAACACTAAAGTCTGAAGATGGCATTATGCAAGAACAGATTATGCAGAGAAT  
 GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTGTCCGGAACATTACAATGGCTTCTGCATGCAT  
 GGGAAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTGCAGGTGTGATGCTGGTTACTGGACAAACACTGT  
 GAAAAAAAGGACTACAGTGTCTACGTTGCTGTTCCGGCTGTACGATTCACTGCTTAATCGCAGCTGTG  
 ATTGGAAACAATTCAAGATTGCTGTCATCTGTGTTGGTGCATCACAGGAAATGCCAGAACAGA  
 ATTACAGACAGAACAGAAATACAGGGCACTACAGTTCAGACAATACAAGAGCGTCCACGGGTTAATC**TAA**  
 AGGGAGCATGTTCACAGTGGCTGGACTACCGAGAGCTGGACTACACAATACAGTATTATAGACAAAAGAATAA  
 GACAAGAGATCTACACATGTTGCCTGCAATTGTGTTGTAATCTACACCAATGAAAACATGTACTACAGCTATATT  
 GATTATGTATGGATATATTGAAATAGTATACTACATTGTCTGATGTTTCTGTAATGAAATAAAACTATTATA  
 TCACACAATATAGTTTCTTCCATGTATTGTTATATATAATAACTCAGTGTGAG

**FIGURE 5**

TTCTGCTATAGAGATGGAACAGTATATGAAAGCTCCCAAGAAAGTGAAGAGAGGAAATTGAAAATTGTGAGTG  
 GACCTCTGATACTGCTCCTCGTGGAAAAGGGAAAGAACTGCATGCATATTATTACAGCGCCTATATT  
 AAAGGATATTCTGGTATCTTGGAAAGTGTCCGTATC**ATGGAATCAATCTCTATGATGGAAAGCCCTAAGAGCCT**  
 TAGTGAAACTGTGTTACCTAATGGCATAAATGGTATCAAAGATGCAAGGAAGGTCACTGTAGGTGTGATTGAAAG  
 TGGAGATTTGCCAAATCCTGACCATTGACTTATTAGATGCGGCTATCATGTGGTCAAGGAAGTAGAAATCC  
 TAAGTTGCTCTGAATTTTCCTCATGTGGTAGATGTCACTCATGAAGATGCTCTCACAAAACAAATAT  
 AATATTGTTGCTATACACAGAGAACATTACCTCCCTGTGGGACCTGAGACATCTGCTTGTGGTAAATCCT  
 GATTGATGTGAGCAATAACATGAGGATAAACAGTACCCAGAATCCAATGCTGAATATTGGCTTATTATCCC  
 AGATTCTTGATTGTCAAAGGATTAATGTTGTCAGCTTGGGCACTTCAGTTAGGACCTAAGGATGCCAGCCG  
 GCAGGTTATATATGCAGCAACAATTCAAGCGCAGAACAGGTTATTGAACCTGCCGCCAGTTGAATTTCAT  
 TCCCATTGACTTGGGATCCTTATCATCAGCCAGAGAGATTGAAAATTACCCCTACGACTCTTACTCTGGAG  
 AGGGCCAGTGGTAGCTATAAGCTTGGCACATTTCCTTATTGTCAGAGATGTGATTCACT  
 ATATGCTAGAAACCAACAGAGTGAACCTTACAAAATTCTATAGAGATTGTGAATAAAACCTACCTATAGTTGC  
 CATTACTTGCTCTCCCTAGTATACCTGCAGGTCTCTGGCAGCTGCTTACACTTATTACGGCACCAAGTA  
 TAGGAGATTCCACCTTGGTAGGAAACCTGGTTACAGTGTAGAAAACAGCTTGGATTACTAAGTTTTCTCGC  
 TATGGTCATGGCCTACAGCCTCTGCTTACCGATGAGAAGGTCAAGAGAGATTGTTGAGAATTGAAATGTATATCTCCT  
 TGGCATAATGAGCCTGGCTACTTCCCTGGCAGTCACTTCTATCCCTCAGTGAGCAATGCTTAAACTG  
 GAGAGAATTCACTTATTCACTGAGTACACTTGGATATGTCGCTCTGCTCATAAGTACTTCCATGTTAATT  
 TGGATGGAAACGAGCTTGAGGAAGAGTACTACAGATTATACACCACCAACTTGGCTTGTCTGTT  
 GCCCTCAATTGTAATTCTGGATCTTGCAGCTTGCAGATAACCCAGACT**TGA**GCTGGAACCTGGAATTGCTTCC  
 TATTGACTCTACTTCTTAAAGCGGCTGCCATTACATTCCCTAGCTGCTTGCAGTTAGGTGTACATGTGAC  
 TGAGTGTGGCAGTGGATATAACAGGAGCCCTGGCAGCTGCTCCAGAGGATCAAAGCCACACCCAAAGAGTAAGGCAG  
 ATTAGAGACCAGAAAGACCTTGACTACTTCCACTGCTTTCTGCATTAAAGCCATTGAAATCTG  
 GGTGTGTTACATGAAGTGAAAATTAAATTCTTCTGCCCTCAGTTCTTATCCTGATACCATTAAACACTGCTG  
 AATTAACTAGACTGCAATAATTCTTCTTTGAAAGCTTTAAAGGATAATGTGCAATTACATTAAATTGATT  
 TTCCATTGTCATTAGTTATACCTCATTCTGCCTGATCTTCATTAGATATTGTATCTGCTTGGAAATATA  
 TTATCTTCTTTAACTGTGTAATTGGTAATTACTAAAACCTGTAATCTCCAAATATTGCTATCAAATTACAC  
 ACCATGTTCTATCATTCTCATAGATCTGCCTATAAACATTAAATAAAAGTACTATTAAATGATTAACTT  
 CTGTTTGGAAAAA

## **FIGURE 6**

MASLGLQLVGYILGLLGLTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCDIYSTLLGLPA  
DIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGLGFIPVAWNHLHGILRDFYSP  
LVPDSMKFEIGEALYLGISSILFSLIAGIILCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYS  
LTGYV

**Signal sequence.**

amino acids 1-24

**Transmembrane domains.**

amino acids 82-102, 120-140, 160-180

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 216-224

**N-myristoylation sites.**

amino acids 17-22, 20-25, 60-65, 101-106, 128-133, 167-172, 178-183

**PMP-22/EMP/MP20/Claudin family.**

amino acids 4-181

**FIGURE 7**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIGPRKQ  
LCDGELDCPLGEDEEHCVKSFPPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGYSRAVE  
IGPDQDLDVVEITENSQELRMRNSSGPGCLSGSLVSLHCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVC  
GGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGT  
VRPICLFFFDEELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGV  
DTCQGDGGPLMYQSDQWHVVGIVSWGYPGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain.**

amino acids 33-60

**Trypsin.**

amino acids 200-424

**Kringle domain proteins.**

amino acids 225-242, 376-388

**Apple domain proteins.**

amino acids 199-239, 196-236, 237-270, 298-328, 368-401, 367-400, 403-430

**LDL-receptor class A.**

amino acids 70-89

**CUB domain proteins.**

amino acids 397-406

**FIGURE 8**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG  
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF  
SMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVSVLYNVTINNTYSC  
MIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYIMLK

**Signal peptide.**

amino acids 1-28

**Transmembrane domain.**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

**N-myristylation sites.**

amino acids 52-58, 126-132, 188-194

**Immunoglobulin domain.**

amino acids 49-132

## **FIGURE 9**

MVLWESPRQCSSWTLCEGFCWLLLLPVMLLIVARPVKLAAFPPTSLSDCQPTGWNCSGYDDRENDLFLCDNTCK  
FDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQAACKQQSEILVVSEGSCATDAGSGSGDGVHEG  
SGETSQKETSTCDICQFGAECDEDAEDVWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLG  
RCQDNNTTTTKSEDGHYARTDYAENANKLEESAREHHIPCPHYNGFCMHGKCEHSINMQEPSCRCDAGYTGQHC  
EKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQKQNTGHYSSDNTRASTRLI

**N-glycosylation sites.**

amino acids 55-58, 230-233, 365-368

**Glycosaminoglycan attachment sites.**

amino acids 141-144, 143-146

**Tyrosine kinase phosphorylation site.**

amino acids 236-242

**N-myristoylation sites.**

amino acids 133-138, 140-145, 142-147, 146-151, 150-155

**EGF-like domain cysteine pattern signature.**

amino acids 289-301

**Kazal-type serine protease inhibitor domain.**

amino acids 91-135, 182-227

## **FIGURE 10**

MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPFASEFFPHVVD  
VTHHEDALTKTNIIFVAIHREHYTSIWDLRHLLVGKILIDVSNNMRINQYPSNAEYLASLFPDSLIVKGFNVVS  
AWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIIDLGSLSAREIENPLRLFTLWRGPVVVAISLATF  
FFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPIVAILLISLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLIQ  
CRKQLGLLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNNEEVWRIEMYISFGIMSLGLLSLLA  
VTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYWKRAFEEYYRFYTPPNFVLALVLP SIVILDLLQLC  
RYPD

**Transmembrane domains.**

amino acids 210-230, 257-277, 299-319, 359-379, 393-413, 428-448

**N-glycosylation site.**

amino acids 256-259

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 29-32

**Tyrosine kinase phosphorylation site.**

amino acids 416-424

**N-myristoylation sites.**

amino acids 8-13, 24-29, 34-39, 193-198, 274-279